

In the Specification:

Please amend the paragraphs on page 5, line 15–30 of the specification as follows:

Figure 2A shows protein multiple sequence alignment of the GLUTn (~~n=1, 5, 8~~n=1, 2, 3, 4, 5, 8, SEQ ID NOS: 38–43 respectively) family with the novel GLUT10 transporter (SEQ ID NO: 2). The alignment was generated using the pileup program (Genetics Computer Group, alignment penalties gap=10, extension=2) and ClustalX. Residues with blue background are identical to the consensus; green background are conserved residues with above average non-identity matrix scores; yellow residues are conserved with below average scores; white are neutral or non-conserved. Putative transmembrane domains were predicted using HMMTOP and TMHMM programs and are overlined. The long exofacial Loop9 between TMD9 and TMD10 separates two conserved blocks near GLUT10 residues 350 and 390.

Figure 2B depicts the approximate phylogram of the GLUT family. Annotated distances are in substitutions per 100 residues. The unrooted phylogram was generated using the GCG distances program under a Kimura protein substitution model from the **Figure 2A** multiple sequence alignment, and reconstructed using a UPGMA method. The sequences used are ~~P111666~~ SwissProt Accession Nos. P11166 (GLUT1, SEQ ID NO: 38), P11168 (GLUT2, SEQ ID NO: 39), P11169 (GLUT3, SEQ ID NO: 40), P14672 (GLUT4, SEQ ID NO: 41), P22732 (GLUT5, SEQ ID NO: 42), and EMBL Translation No. CAB89809 (GLUT8, SEQ ID NO: 43).

At the end of the specification, please add the enclosed Substitute Sequence Listing, independently numbered pages 1–27.